AMENDMENTS TO THE CLAIMS

Pursuant to 37 C.F.R. § 1.121 the following listing of claims will replace all prior versions, and listings, of claims in the application.

1. (Currently Amended) A computer-based system for measuring the similarity between protein profile matrices stored in a computer readable medium to predict a protein three-dimensional structure, wherein

each profile matrix comprises a group of profile columns containing occurrence probabilities of every amino acid type at a respective locations of amino acid residues in a multiple alignment in which amino acid sequences of a plurality of related proteins are multiply aligned,

said system comprises:

(a)   means for preparing and storing in the computer readable medium two profile matrices of a query profile matrix formed based on a plurality of proteins including proteins having three-dimensional structures to be predicted and a subject profile matrix formed based on a plurality of proteins having known three-dimensional structures retrieved from the computer readable medium;

(b)   means for calculating and storing in the computer readable medium correlation coefficients between the respective profile columns in said query profile matrix and the respective profile columns in said subject profile matrix with respect to full or partial combinations of both the respective profile columns; and

(c)   means for forming a score matrix comprising said correlation coefficients and storing the score matrix in the computer readable medium; and

(d)   means for outputting at least one candidate for the predicted protein three-dimensional structure based on the results of the score matrix.

2. (Original): A system for predicting a protein three-dimensional structure characterized in using a score matrix formed through a system set forth in claim 1.

3. (Currently Amended): An executable program embodied in a computer readable medium for enabling a computer to function as a system for measuring the similarity between protein profile matrices to predict a protein three-dimensional structure, wherein

each profile matrix comprises a group of profile columns containing occurrence probabilities of every amino acid type at a respective locations of amino acid residues in a multiple alignment in which amino acid sequences of a plurality of related proteins are multiply aligned,

said system comprises:

(a)   means for preparing two profile matrices of a query profile matrix formed based on a plurality of proteins including proteins having three-dimensional structures to be predicted and a subject profile matrix formed based on a plurality of proteins having known three-dimensional structures;

(b)   means for calculating correlation coefficients between the respective profile columns in said query profile matrix and the respective profile columns in said subject profile matrix with respect to full or partial combinations of both the respective profile columns; ~~and~~

(c)   means for forming a score matrix comprising said correlation coefficients; and

(d)   means for outputting at least one candidate for the predicted protein three-dimensional structure based on the results of the score matrix.

4. (Original): A computer-readable recording medium storing a program set forth in claim 3.

5. (Currently Amended): A method for measuring the similarity between protein profile matrices to predict a protein three-dimensional structure, wherein

each profile matrix comprises a group of profile columns containing occurrence probabilities of every amino acid type at a respective locations of amino acid residues in a multiple alignment in which amino acid sequences of a plurality of related proteins are multiply aligned,

said method comprises:

        (a)   preparing two profile matrices of a query profile matrix formed based on a plurality of proteins including proteins having three-dimensional structures to be predicted and a subject profile matrix formed based on a plurality of proteins having known three-dimensional structures;

        (b)   calculating correlation coefficients between the respective profile columns in said query profile matrix and the respective profile columns in said subject profile matrix with respect to full or partial combinations of both the respective profile columns; ~~and~~

        (c)   forming a score matrix comprising said correlation coefficients; and

        <u>(d)   outputting at least one candidate for the predicted protein three-dimensional structure based on the results of the score matrix</u>.